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October 5, 2002, 03:30:35 ; Search time 1713.89 Seconds (without alignments) 3709.145 Million cell updates/sec
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

Description	W72837 2d57g12.r1 W72838 2d57g12.s1 AW070916 xa31d01.x	BF742809 IL2-BT080 AII39456 qc20g01.x BG202312 RST21668	BG092421 CN1-BT073 BG092421 CN1-BT073 BG185269'-RST4208 A R75793 Y121 f09.r1	ACO 94 0.50; ACO 94 0.50; ACO 94 0.50; AM 7 6 0.4 4 QVQ. BT 0.10 AAA 9 0.00 9.50; BE 18 6 0.13 ACO 3 ACO 95 ACO 9	AI127172 qb99a08.x
SUMMARIES	W72837 W72838 AW070916	BF/42809 AI139456 BG202312 BG218084	BE092421 BE185269 R75793 A2694036	BG202313 AW176044 AA340069 BE186013 BE926938	7/1/7118
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ALIGNMENTS

RESULT 1 W72837 LOCUS DEFINITION ACCESSION VERSION	W72837 436 bp mRNA linear EST 16-OCT-1996 2d57g12.rl Soares_fetal_heart_NbHH19W Homo sapiens cDNA clone INAGE:344806 5' similar to contains element MER40 repetitive element; mRNA sequence. W72837 W72837.1 GI:1382813
KEYWORDS SOURCE ORGANISM REFERENCE AUTHORS	human. Humo sapiens Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostoml; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo. I (bases 1 to 436) Hillier,L., Clark,N., Dubuque,T., Elliston,K., Hawkins,M., Holman,M., Kuckaba,T., Le,M., Lennon,G., Marram,P., Parsons,J., Mitkin I Bohleton of Consort
TITLE JOURNAL COMMENT	The WashU-Merck EST Project The WashU-Merck EST Project Unpublished (1995) Contact: Wilson RK Washington University School of Medicine 4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108 Tel: 314 286 1800
FEATURES SOURCE	Email: essewatson.wustl.edu This clone is available royalty-free through LLNL; contact the IMAGE Consortium (info@image.llnl.gov) for further information. Insert Length: 508 Ext Error: 0.00 Seq primer: mob.REGA+ET. Location/Qualifiers 1. 436 /organism="Homo sapiens"
	/db_xref="GDB:1270181" /db_xref="taxon:9606" /clone="IMACE:344806" /clone_lib="Soares_fetal_heart_NbHH19W" /sex="unknown" /dev_stage="19 weeks" /lab_host="DH10B (ampicillin resistant)"

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1 (bases I to 432)

1 (hases I to 600)

2 (hases I to 600)

3 (hases I to 600)

4 (hases I to 600)

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Pred. No. 7.6e-101;
0; Mismatches 3;
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4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
Feb: 314 286 1800
Fax: 314 286 1810
Email: est@watson.wustl.edu
This clone is available royalty-free through LLNL; contact the
IMAGE Consortium (info@image.llnl.gov) for further information.
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Pred. No. 1.8e-93;
): Mismatches 3; Indels 2;
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/db_xref="GDB:1270181"
/db_xref="taxon:9606"
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/sex="unknown"
Contact: Wilson RK
Washington University School of Medicine
                                                                                                                                   Seq primer: mob.REGA+ET
High quality sequence stop: 394
Location/Qualifiers
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98.8%;
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Eukaryota; Metazoa: Chordata; Craniata; Vertebrata; Euteleostomi:
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 423)
Dias Neto,E., Garcia Correa,R., Verjovski-Almeida,S., Briones,M.R.,
Nagai,M.A., da Silva,W. Jr., Zago,M.A., Bordin,S., Costa,F.F.,
Goldman,G.H., Carvalho,A.F., Matsukuma,A., Baia,G.S., Simpson,D.H.,
Brunstein,A., deOliveira,P.S., Bucher,P., Jongeneel,C.V., O'Hare
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /dev_arge="Andle"
/note="Organ: breast; Vector: pucl8; Site_1: Smal; Site_2:
Smal; A min!-library was made by cloning products derived
from ORESTES POR (U.S. Letters Patent application No. 196
/16 - Ludwig Institute for Cancer Research) profiles
into the pUC 18 vector. Reverse transcription of tissue
mRNA and cDNA amplification were performed under low
stringency conditions.

a 123 c 87 g 124 t
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Tel: +55-11-2704922
Fax: +55-11-2707001
Email: asimpson@ludwig.org.br
This sequence was derived from the FAPESP/LICR Human Cancer Genome Project. This entry can be seen in the following URL (http://www.ludwig.org.br/scripts/gethtml2.pl?tl=IL26t2=IL2-BT0807-041000-176-G036t3-2000-10-046t4=1)
Seq primer: puc 18 forward
High quality sequence stop: 421.
                                                                                                                                                                                       EST 10-JAN-2001
                                                                                                                                                                                  BF742809
LL2-BT0807-041000-176-G03 BT0807 Homo sapiens cDNA, mRNA sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Contact: Simpson A.J.G.
Laboratory of Cancer Genetics
Ludwig Institute for Cancer Research
Rua Prof. Antonio Prudente 109, 4 andar, 01509-010, Sao Paulo-SP,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Simpson, A. \enskip J. \\ Shotgun sequencing of the human transcriptome with ORF expressed \\
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20202663
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); Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /organism="Homo sapiens"
/db_xref="taxon:9606"
/clone_lib="BT0807"
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                                                   AW070916 420 bp mRNA linear EST 20-OCT-2000 xa31d01.xl NCI_CGAP_Br18 Homo sapiens cDNA clone IMAGE:2568385 3' similar to contains element TAR1 repetitive element ;, mRNA
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/clone_lib="NCI_CGAP_Br18"
/fissue_type="four pooled high-grade tumors, including two primary tumors and two metastatic to ovary"
/lab_host="DH108"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ;;
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (Dases 1 to 420)
NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
                                                                                                                                                                                                                                                                                                                                                                                        Email: cgapbs-rémail.nih.gov

Tissue Procurement: Chris Moskaluk, M.D., Ph.D., Michael R.
Enmert-Buck, M.D., Ph.D. cDNA Library Preparation: Life
Forhologies, Inc. cDNA Library Preparation: Life
Technologies, Inc. cDNA Library Prayed by: Christa Prange, The
I.M.A.G.E. Consortium DNA Sequencing by: Washington University
Chome Sequencing Center
Clone distribution: NGI-CGAP Clone distribution information can the found through the I.M.A.G.E. Consortium/LLNL at:
Insert Length: 545 Std Error: 0.00
Seq primer: -400P from Gibco.
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76 c 116 g 109 t
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Pred. No. 2.8c-90;
0; Mismatches 7;
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Unpublished (1997)
Contact: Robert Strausberg, Ph.D.
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/db_xref="taxon:9606"
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                                                                                                                                 AW070916
AW070916.1 GI:6025914
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98.1%;
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Matches 406; Conserv
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/lab_host="0H10B (ampicillin resistant)"
/lab_host="0H10B (ampicillin resistant)"
/lab_host="0H10B (ampicillin resistant)"
/lab_host="0H10B (ampicillin resistant)"
/lab_host="0H10B (ampicillin resistant)
/lab_host="0H10B (am
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Ali39456 1 GI:3645428
EST.
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Eukaryota: Metazoa: Chordata: Craniata: Vertebrata; Eut@leostomi;
Mammalia: Eutheria: Primates: Catarrhini; Hominidae; Homo.
1 (bases 1 to 402)
NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Contact: Robert Strausberg, Ph.D.
Email: cgapbs-rémail.nh.gov
This clone is available royalty-free through LLNL; contact the IMAGE Consortium (info@image.llnl.gov) for further information.
Insert Length: $10 Std Error: 0.00
Seq primer: -40ml3 fwd. ET from Amersham
High quality sequence stop: 398.
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Pred. No. 3e-87;
0; Mismatches 5; Indels
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/clone_lib="Soares_fetal_heart_NbHH19W"
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    402
/organism="Homo sapiens"
/db_xref="taxon:9606"

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98.5%;
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Unpublished (1997)
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Gaps

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5; Indels

Best Local Similarity 98.5 Matches 393; Conservative

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/organism="Homo sapiens"
/db_xref="taxon:9606"
/dlone_lib="Athersys RAGE Library"
/cell_lib="HTI080"
/cote="See 'Creation of Genome-wide Protein Expression
Libraries using Random Activation of Gene Expression
Libraries using Random Activation of Gene Expression
Libraries using Random Activation of Gene Expression
in Uppe indicated is HTI080, since a random activation
method was used, these sequence tags are not necessarily
expressed in HTI080 under normal circumstances."
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RST21668 Athersys RAGE Library Homo sapiens CDNA, mRNA sequence.
BG202312
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Harrington, J.J., Sherf,B., Rundlett,S., Jackson,P.D., Perry,R., Cain,S., Leventhal,C., Thornton,M., Ramachandran,R., Whittington,J., Lerner,L., Costanzo,D., McElligott,K., Boozer,S., Mays,R., Smith,S., Larner,L., Costanzo,D., McElligott,K., Boozer,S., Mays,R., Smith,J., Danzig,J. and Ducar,M. Cothren,K., Lo,K., Offenbacher,J., Danzig,J. and Ducar,M.
Creation of genome wide protein expression libraries using random activation of gene expression
Nat. Biotechnol. 19 (5), 440-445 (2001)
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Tel: 216 431 9900
Fax: 216 361 9596
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             High quality sequence stop: 464. Location/Qualifiers
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Bukaryota, Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Bukaryota; Metazoa; Chordata; Catarrhini; Hominidae; Homo.

1 (bases 1 to 376)
Harrinton, J.G., Sherf, B., Rundlett, S., Jackson, P.D., Perry, R.,
Harrinton, J.G., Thornton, M., Ramachandran, R., Whitfangton, J.
Lener, L., Coctanco, D., McElligott, K., Boozer, S., Mays, R.,
Erner, L., Cockanco, D., McElligott, K., Boozer, S., Mays, R.,
J., Danzig, J. and Ducar, M., Hess, J., Cothren, K., Lo, K., Offenbacher
Creation of genome-wide protein expression libraries using random activation of gene expression

Nat. Biotechnol. 19 (5), 440-445 (2001)
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/db_xref="taxon:9606"
/clone_lib="Athersys RACE Library"
/cell_line="H11806"
/inche="See 'Creation of Genome-wide Protein Expression
Libraries using Random Activation of Gene Expression
Nature Biotechnology, in press. Note that even though the
cell type indicated is H11080, since a random activation
method was used, these sequence tags are not necessatily.
                                                                                                                     280
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               DB 10; Length 464;
                                         Indels
Score 345,2; DB 10;
Pred, No. 1,6e-78;
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3201 Carnegie Ave, Cleveland, OH 44115, USA
Tel: 216 431 9900
Email: Scain@athersys.com
High quality sequence stop: 376.
                            Pred. No. 1.6e
0; Mismatches
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            73.38;
97.68;
                                      Matches 361; Conservative
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mRNA sequence.
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Fax: +55-11-2707001
Email: asimpson@ludwig.org.br
This sequence was derived from the FAPESP/LICR Human Cancer Genome
Project. This entry can be seen in the following URL
(http://www.ludwig.org.br/scripts/gethtml2.pl?tl-&t2-CMl-BT0738-250
Seq primer: puc 18 forward
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Ludwig Institute for Cancer Research
Rua Prof. Antonio Prudente 109, 4 andar, 01509-010, Sao Paulo-SP,
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Eutele
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 345)
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normal circumstances.
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20202663
                                                                                              Length 376;
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CM1-BT0738-250400-200-c12 BT0738 Homo sapiens cDNA,
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Pred. No. 7e-75;
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     expressed in HT1080 under 103 c 67 q 104
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95.6%;
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Email: scain@athersys.com
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Fax: 216 361 9596
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[ bases 1 to 391)

Harrington, J. J., Sherf, B., Rundlett, S., Jackson, P.D., Perry, R., Cain, S., Leventhal, C., Thornton, M., Ramachandran, R., Mhittington, J., Lerner, L., Costanzo, D., McElligott, K., Boozer, S., Mays, R., Smith, J., Danzig, J. and Ducar, M. Hess, J., Cothren, K., Lo, K., Offenbacher, J., Danzig, J. and Ducar, M.

Creation of genome wide protein expression libraries using random activation of gene expression

Nat. Blotechnol. 19 (5), 440-445 (2001)
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3201 Carnegie Ave, Cleveland, OH 44115, USA
Tel: 216 431 9900
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Corganism-"Homo sapiens"
/db_xref="taxon:9606"
/clone_lib-"BR0738"
/dev_stage="Adult"
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77 c 103 g
High quality sequence start: 9
High quality sequence stop: 345.
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/organism="Homo saplens"
/db_xref="taxon:9606"
/clone_lib="Athersys RAGE Library"
/cell_line="#171800"
/note="See 'Creation of Genome-wide Protein Expression
Libraries using Random Activation of Gene Expression
/ Nature Biotechnology, in press. Note that even though the
cell type indicated is #11080, since a random activation
method was used, these sequence tags are not necessarily
expressed in #11080 under normal circumstances."

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Hillier, L., Clark, N., Dubuque, T., Elliston, K., Hawkins, M., Holman, M., Hultman, M., Kucaba, T., Le, M., Lennon, G., Marra, M., Parsons, J., Rifkin, L., Rohlfing, T., Soares, M., Tan, F., Trevaskis, E., Waterston Tre Washu Merck EST Project Unpublished (1995)
Contact: Wilson RK
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        accactgctcgtaaagacattccagttttacccaaatgggttgggggatctcccgaatggt
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    110 ACCACTGCTCGTAAAGACATTCCAGTTTTACCCAAATGGGTTGGGGATCTCCCGAATGGT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     agagtgtgtccctgagatggaatcagcttgagtcttctgcaattgggtcacaactattca
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Score 309.8; DB 10; Length 391;
Pred. No. 2.1e-69;
0; Mismatches 8; Indels 2;
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4444 Forest Park Parkway, Box 8501, St. Louls, MO 63108
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aaaataactatgagc 461
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                                                               REFERENCE
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                                                                                                                     . '6
                                                                                                                                                                                                                                                                                   double-stranded cDNA was ligated to Eco RI adaptors (Pharmacia), digested with Not I and cloned into the Not I and Eco RI sites of a modified pT7T3 vector (Pharmacia). Library went through one round of normalization to a Cot = 230. Library constructed by Bento Soares and M.Fatima Bonaldo."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         GSS 18-DEC-2000
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Az694036
AZ694036.1 GI:11878955
                    High quality sequence stops: 307
Source: IMAGE Consortium, LLNL
This clone is available royalty-free through LLNL; contact the
IMAGE Consortium (info@image.llnl.gov) for further information.
Insert Length: 516 Std Error: 0.00
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           68 gtactcttgggagtttccatctttctggtctctgcccagaatccgacaacagctgctcca 127
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        62 GNACTCTTGGGAGTTTCCATCTTTTGGGCTCTCTGCCCAGAATCCGACAACAGCTGCTCCA 121
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         128 gctgacacgtatccagctactggtcctgctgatgatgaagcccctgatgctgaaaccact 187
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       248 actgctcgtaaagacattccagttttacccaaatgggttggggatctcccgaatgg--ta 305
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                242 ACTGCTCGTAAAGACATTCCAGTTTTACCCAAATGGGTTGGGGATCTCCCGAATGGGTAG 301
                                                                                                                                                                                                                                                                                                                                                                                                                                                          6
                                                                                                                                                                                                                                                                                                                                                                                                           Score 308.8; DB 10; Length 403;
Pred. No. 3.7e-69;
0; Mismatches 15; Indels 9;
                                                                                                                                                                                                                                                                                                                                                              3 others
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       362 TTCATGCTTCCTGTGGATTTTCATCCAATTAATTNACCT 400
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          361 ttcatgcttcctgtg--atttcatccaactacttacctt 397
                                                                                                                                                                                                                                                                                                                                                            116 t
                                                                     Insert Length: 516 Std Error:
Seq primer: M13RP1
High quality sequence stop: 307
Location/Qualifiers
1.403
Email: est@watson.wustl.edu
Insert Size: 516
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                                                                                                                                                                                                                                                                                                                                                                                                            65.6%;
94.0%;
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Best Local Similarity
Matches 375; Conserv
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AZ694036
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Aurora Biosciences Corp.

Aurora Biosciences Corp.

11010 Torreyana Road, San Diego, CA 92121, USA
Tel: 8584046719

Email: henkelg@aurorabio.com
Pools of cells were isolated from a GenomeScreen(TM) library. The
library of cells was generated by retroviral integration of a gene
tagging element consisting of: 1) A promoterless beta-lactamase
proceeded by a splice acceptor as a reporter for gene expression;
2) A promoter diving neomycin resistance followed by a splice
donor to trap downstream exons. 3' RACE from neomycin gene was
performed using total RNA from isolated pools. Output was shotgun
cloned in pAmp-1 and used to transform DH5-alpha competent
bacteria. 5' ends of reported sequences were immediately preceded
by splice donor from the trapping construct.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /note="Organ: peripheral blood; Vector: pAmp-1; 3' RACE of total RNA from genetrap pools; shotgun clone in pAmp-1 and total RNA from DH5-alpha competent bacteria."

88 c 94 t
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                                                                                                      Bernardino, A.
      Chordata; Craniata; Vertebrata; Euteleostomi;
Primates; Catarrhini; Hominidae; Homo.
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/db_xref="taxon:9606"
/clone_lib="Genetrap HL-60 Human Promyelocytic Leukemia
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                                                                                                Pratt, E., Huang, D., Riley, M.,
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; R
Mammalia; Eutheria; Primates; Catarrhini; Hominidae;
I (bases 1 to 314)
Henkel,G., Liyanage,M., Pratt,E., Huang,D., Riley,M.,
Durick,K. and Pollok,B.
Con-trap tags from a HL-60 GenomeScreen(TM) Library
Unpublished (2000)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /tissue_type="acute promyelocytic leukemia"
/cell_type="promyeloblast"
/cell_line="HL-60"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Location/Qualifiers
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93
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                         BG202313 343 bp mRNA linear EST 21-APR-2001
RS721669 Athersys RAGE Library Homo sapiens CDNA, mRNA sequence.
                                                                                                                                          Harrington, J. J., Sherf, B., Rundlett, S., Jackson, P.D., Perry, R., Cain, S., Leventhal, C., Thornton, M., Ramachandran, R., Whittington, J., Lerner, L., Costanzo, D., McElligott, K., Boozer, S., Mays, R., Smith, E., Veloso, N., Klika, A., Hess, J., Cothren, K., Lo, K., Offenbacher, J., Danzig, J. and Ducar, M.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                         /note="See 'Creation of Genome-wide Protein Expression Libraries using Random Activation of Gene Expression', Nature Biotechnology, in press. Note that even though the cell type Indicated is HT1080, since a random activation method was used, these sequence tags are not necessarily expressed in HT1080 under normal circumstances."
                                                                                                     Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /organism="Homo sapiens"
/db_xref="taxon:9606"
/clone_lib="Athersys RAGE Library"
/cell_line="HT1080"
                                                                                                                                                                                                                                                                                                          3201 Carnegie Ave, Cleveland, OH 44115, USA
Tel: 216 431 9900
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           63.5%; Score 299.2; DB lilarity 93.3%; Pred. No. 1.1e-66; Conservative 0; Mismatches 22
                                                                                                                                                                                                                                                     Nat. Biotechnoí. 19 (5), 440-445 (2001)
21227151
                                                                                                                                                                                                                                                                                                               Jaco Control of 131 9900
Fax: 216 431 9900
Fax: 216 361 9596
Email: scain@athersys.com
High quality sequence stop: 343.
Location/Qualifiers
                                                                                                                                                                                                                                          activation of gene expression
                                                                 BG202313.1 GI:13724000
                                                                                                                                                                                                                                                                                Contact: Scott J. Cain
Athersys, Inc.
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Matches 321;
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/organism="Homo sapiens"
/db_xref="taxon:9606"
/db_xref="taxon:9606"
/dclone_lib="BT00103"
/dev_stage="Adult"
/note="Organ: breast; Vector: pucl8; Site_1: Sma1; Site_2: Sma1; A min1-library was made by cloning products derived from ORESTES POR (U.S. Letters Patent application No. 196
/716 - Ludwig Institute for Cancer Research) profiles into the pUC 18 vector. Reverse transcription of tissue mNNA and cDNA amplification were performed under low
AW176044 313 bp mRNA linear EST 16-NOV-1999
QVO_ET0103-270899-008-f12 BT0103 Homo sapiens CDNA, mRNA sequence.
                                                                                                                                                                                                                                                                                                                                                                                             Fax: +55-11-2707001
Email: asimpson@ludwig.org.br
This sequence was derived from the FAPESP/LICR Human Cancer Genome
Project. This entry can be seen in the following URL
(http://www.ludwig.org.br/scripts/gethtml2.pl?tl=QV0&t2=QV0-BT0103-
27089g-008-f12&t3=199g-08-27&t4=1)
Seq primer: puc.18 forward
High quality sequence start: 7
High quality sequence stop: 313.
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                                                                                                                                                Enteleostomi;
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Eutelo
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ::
                                                                                                                                                                                                                                                                       Contact: Simpson A.J.G.
Laboratory of Cancer Genetics
Ludwig Institute for Cancer Research
Rua Prof. Antonio Prudente 109, 4 andar, 01509-010,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           62.4%; Score 294; DB 9; Length 313;
llarity 98.1%; Pred. No. 2.3e-65;
Conservative 0; Mismatches 5; Indels
                                                                                                                                                                                      1 (bases 1 to 313)
HGGP http://www.ludwig.org.br/ORESTES.
The FAPESS/LICR Human Cancer Genome Project Unpublished (1999)
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                                     AW176044
AW176044.1 GI:6442081
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DEFINITION

ACCESS ION VERSION KEYWORDS SOURCE

ORGANISM

REFERENCE AUTHORS

7

RESULT 1

14

9

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BE186013
CM1 HT0738-250400-199-bll HT0738 Homo sapiens CDNA, mRNA sequence.
BE186013
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Email: asimpsoneludwig.org.br
This sequence was derived from the FAPESP/LICR Human Cancer Genome
Project. This entry can be seen in the following URL
(http://www.ludwig.org.br/scripts/gethtml2.pl?tl=&t2=CMI-HT0738-250
400-199-bli&t3=2000-04-25&t4=1)
Seq primer: puc 18 forward
High quality sequence start: 4
High quality sequence stop: 316.
Location/Qualifiers
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/db_xref="taxon:9606"
/db_xref="taxon:9606"
/dclone_lib="HT0738"
/dev_stage="Adult"
/note="Organ: head_neck; Vector: puc18; Site_1: Smal;
Site_2: Smal; A mini-library was made by cloning products
Garlved from ORESTES PCR (U.S. Letters Patent application
No. 196,716 - Ludwig Institute for Cancer Research)
profiles into the pUC 18 vector. Reverse transcription of
tissue mRNA and cDNA amplification were performed under
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1 (bases 1 to 316)
Dias Neto, E., Garcia Correa, R., Verjovski-Almeida, S., Briones, M.R., Nagai, M.A., Garcia Correa, R., Sago, M.A., Bordin, S., Costa, F.F., Goldman, G.H., Carvalho, A.F., Matsukuma, A., Baia, G.S., Simpson, D.H., Brunstein, A., deoliveira, P.S., Bucher, P., Jongeneel, C.V., O'Hare, M.J., Soares, F., Brentani, R.R., Reis, L.F., de Souza, S.J. and
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Rua Prof. Antonio Prudente 109, 4 andar, 01509-010, Sao Paulo-SP,
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Eulele
Mammalla; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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Pred. No. 5.3e-62;
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Laboratory of Cancer Genetics
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Best Local Similarity 97.8%;
Matches 306; Conservative (
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1 (bases 1 to 294)

2 Adams, W.D., Kerlavage, A.R., Fleischmann, R.D., Fuldner, R.A., Bult C.J., Lee, N.H., Kirkness, E.F., Weinstock, K.G., Gocayne, J.D., White, O., Sutton, G., Blake, J.A., Earle-Hughes, J., Fine, L.D., Fitzgerald Cline, T.R., Cotton, M.D., Earle-Hughes, J., Fine, L.D., Fitzgerald Chehm, C.L., Hanna, M.C., Heddlom, E., Hinkle, P.S., Jr., Kelley, J.M., Kelley, J.C., Liu, L.-I., Marmaros, S.M., Merrick, J.M., Kelley, J.C., Liu, L.-I., Marmaros, S.M., Merrick, J.M., Shirley, R., Small, K.V., Spriggs, T.A., Utterback, T.R., Weidman, J.F., Li, Y., Bednait, D.D., Cao, L., Cepeda, M.A., Coleman, T.A., Collins, E.J., Dimke, D., Ferrie, A., Fischer, C., Hastings, G.A., H., W., Kunsch, C., Hungjun, J., Li, H., Meissner, P.S., Olsen, H., Raymond, L., Weit, Y.F., Wing, J., Xu, C., Yu, G.L., Ruben, S.M., Dillion, P.J., Fannon, W.R., Rosen, C.A., Haseltine, W.A., Fields, C., Fraser, C.M. and
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Similar to
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for clone availability, additional sequence and expression
information related to this EST, please check the TIGR Human Gene
Index (http://www.tigr.org/tdb/hgl/hgl.html)
                                                                                                                                                                                                                                                                                                                            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
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9712 Medical Center Drive, Rockville, MD 20850 USA
Tel: 3018699056
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/db_xref="ATCC (inhost):141700"
/db_xref="taxon:9606"
/clone_lib="Fetal skin"
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/dev_stage="fetus"
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Bioinformatics
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Pred. No. 8.6e-126;
0; Mismatches 6;
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PCT-US93-04648-15
US-08-770-379-20
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US-08-770-371A-20
US-09-230-371A-20
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Patent No. 631292

GENERAL INFORMATION

APPLICANT: Dumas Milne Edwards, Jean-Baptiste

APPLICANT: Dumas Milne Edwards, Jean-Baptiste

APPLICANT: Bougueleret, Lydie

TITLE OF INVENTION: Complementary DNAS

FILE REFERENCE: GENSET. 021A

CURRENT APPLICATION NUMBER: US/09/247,155A

CURRENT FILING DATE: 1999-02-09

EARLIER PRILING DATE: 1998-02-09

EARLIER PRILING DATE: 1998-04.13

EARLIER FILING DATE: 1998-04.13

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EARLIER PRILING DATE: 1998-04.13

SOFTWARE: PAPELICATION NUMBER: 60/099,273

SEQ ID NOS: 182

LENGTH. 497
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LOCATION: 68..337
LOCATION: 68..337
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NAME/KEY: sig_peptide
LOCATION: 68..124
OTHER INFORMATION: Von Heijne matrix
OTHER INFORMATION: Score 10
OTHER INFORMATION: Seq LVLLGVSIFLVSA/ON
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NAME/KEY: polya_signal
LOCATION: 462..467
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                    GenCore version 4.5
Copyright (c) 1993 - 2000 Com
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TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELEPRONE: 612-305-1217
TELEFRAX: 612-305-1225
INFORMATION FOR SEQ ID NO: 3:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                               13.9%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                      Ouery Match
Best Local Similarity 63.99
                                                                                                                                                                                                      CRGANISM: Homo sapiens US-09-135-994-1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    USA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 55401
                                                                                                                                                                          LENGTH: 477
TYPE: DNA
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APPLICANT: Dong Kyu JIN

TITLE OF INVENTION: Diagnostic Method and Kit for Neuropsychiatric Diseases

TITLE OF INVENTION: Using Trinucleotide Repeats Sequence

FILE REFERENCE: 1942/36

CURRENT APPLICATION NUMBER: US/09/253,691

EARLIER FILING DATE: 1996-02-22

EARLIER FILING DATE: 1996-02-26

NUMBER OF SEQ ID NOS: 3

SOFTWARE: WordPerfect 6.1/Windows

SEQ ID NO 3
                          aaccactgctgctgcaacaactgcgaccactgctgctcctaccactgcaaccaccgctgc 240
                                                                                                                                                        75 tgggagtttccatcttctggtctctgcccagaatccgacaacagctgctccagctgaca 134
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           14.6%; Score 68.6; DB 3;
61.5%; Pred. No. 1.9e-11;
iive 0; Mismatches 69;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence 1, Application US/09135994A
                                                                                                                                                                                                                                                                                                                                                                                                                                             KESULT 2
US-09-253-691-3/C
Sequence 3, Application US/09253691
Patent No. 6124100
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Best Local Similarity 61.5
Matches 110; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   : TYPE: DNA
; ORGANISM: human
US-09-253-691-3
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US-09-135-994-1/C
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99 ctgcccagaatccgacaacagctgctccagctgacacgtatccagctactggtcctgctg 158
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Patent No. 5741645
GENERAL INFORMATION:
APPLICANT: Ranum, Laura P.W.
APPLICANT: Zoghbi, Huda Yi.
APPLICANT: Zoghbi, Huda Yi.
PATELE OF INVENTION: Gene Sequence for Spinocerebellar Ataxia
PATELE OF INVENTION: Type I and Method for Diagnosis
NUMBER OF SEQUENCES: 47
                                                                                                                                                                                                                                                                                                                                                                                                                            Length 477;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CORRESPONDENCE ADDRESS:
ADDRESSEE: Mueting, Reasch, Gebhardt & Schwappach, STREET: 119 No. 5741645th Fourth Street, Sulte 203 CITY: Minneapolis STATE: MN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  COMPOTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/469,802B
FILING DATE: 06-JUN-1995
CLASSIFICATION: 435
ATTORNEY/AGRNT INFORMATION:
NAME: Mueting, Ann M.
REGISTRATION NUMBER: 33,977
REFERENCE/DOCKET NUMBER: 110.00030101
GENERAL INFORMATION:

APPLICANT: Ranum et al.

ITILE OF INVENTION: SCA7 GENE AND METHODS OF USE

FILE REPERENCE: University of Minnesota

CURRENT APPLICATION NUMBER: US/09/135,994A

CURRENT FILING DATE: 1998-08-19

EARLIER FILING DATE: 1997-08-19

NUMBER OF SEQ ID NOS: 14

SOFTWARE: Patentin Ver. 2.0
                                                                                                                                                                                                                                                                                                                                                                                                                         Score 65.4; DB 4;
Pred. No. 1.9e-10;
0; Mismatches 56;
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61 agtoctggtactcttgggagtttccatctttctggtctctgcccagaatccgacaacagc 120
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                                                                                                                                                    APPLICANT: Croce, Carlo
APPLICANT: Canani, Eli
TITLE OF INVENTION: Diagnostics, Therapeutics and Methods for
TITLE OF INVENTION: Detection and Treatment of Acute Leukemias
TITLE OF INVENTION: Resulting from Chromosome Abnormalities in the
NUMBER OF SEQUENCES: 44
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            3: Woodcock Washburn Kurtz Mackiewicz 6 No. 5633135ris
One Liberty Place - 46th Floor
                                                         Length 234;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ZIP: 19103
COMPUTER READABLE FORM:
MEDIUM TYPE: DISKETTE, 3.5 INCH, 1.44 Mb STORAGE
                                                 Ouery Match 13.8%; Score 65; DB 2; DB 2; DB 2t Local Similarity 58.5%; Pred. No. 1.7e-10; Matches 113; Conservative 0; Mismatches 80
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/08/062,443
FILING DATE: 14 MAY 1993
FRIOR APPLICATION DATA:
APPLICATION NUMBER: US/07/971,094
FILING DATE: 30-0CT-92
FRIOR APPLICATION DATA:
APPLICATION NUMBER: US/07/888,830
FILING DATE: 27-MAY-92
FRIOR APPLICATION DATA:
APPLICATION NUMBER: US/07/805,093
FILING DATE: 11-DEC-91
ATTORNEY/AGENT INFORMATION:
WANTENEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                COMPUTER: IBM PS/2
OPERATING SYSTEM: PC-DOS
SOFTWARE: WORDPERFECT 5.1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/320,559
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  NAME: DeLuca, Mark
REGISTRATION NUMBER: 33,229
REFERENCE/DOCKET NUMBER: TJU-0855
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ; Sequence 29, Application US/08320559; Patent No. 5633135; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TELEPHONE: (215) 568-3100
TELEFAX: (215) 568-3439
INFORMATION FOR SEO ID NO: 29:
SEQUENCE CHARACTERISTICS:
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ADDRESSEE: Woodcock
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                                                                                                                                                                                                                                                                            0; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 GENERAL INFORMATION:
APPLICANT: Orr, Harry T.
APPLICANT: Ranum, Laura P.W.
APPLICANT: Chung, Ming-yi
APPLICANT: Cagnbi, Huda Y.
TITLE OF INVENTION: Gene Sequence for Spinocerebellar Ataxia
PACEL FOR INVENTION: Type 1 and Method for Diagnosis
NUMBER OF SEQUENCE: 85
CORRESPONDENCE ADDRESS:
                                                                                                                                                            Score 65; DB 1; Length 234;
Pred. No. 1.7e-10;
0; Mismatches 80; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ADDRESSEE: Mueting, Raasch, Gebhardt & Schwappach, P.A.
STREET: P.O. Box 581415
CITY: Minneapolis
STATE: MN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/267,803B
FILING DATE: 28-JUN-1994
CLASSIFICATION: 435
ATTONNEY/AGENT INPORMATION:
NAME: MCCORMACK, Myra H.
REGISTRATION NUMBER: 36,602
REFERENCE/DOCKET NUMBER: 110.00030120
TELECOMMUNICATION INFORMATION:
TELEPHONE: 612-305-1228
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                : Sequence 3, Application US/08267803B
: Patent No. 5834183
                                                                                                                                                            Ouery Match 13.8%;
Best Local Similarity 58.5%;
Matches 113; Conservative 0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TELEFAX: 612-305-1228
INFORMATION FOR SEQ ID NO: 3:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Floppy disk
LENGTH: 234 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            LENGTH: 234 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ZIP: 55458-1415
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          241 ttctaccactgct 253
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: MOLECULE TYPE: DNA
US-08-469-8028-3
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US-08-267-803B-3/c
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Sequence 29, Application PC/TUS9404496
GENERAL INFORMATION:
APPLICANT: Croce, Carlo
APPLICANT: Canaani, Eli
TITLE OF INVENTION: Diagnostics, Therapeutics and Methods
TITLE OF INVENTION: for Detection and Treatment of Acute Leukemias
TITLE OF INVENTION: Resulting from Chromosome Abnormalities in the All-1
NUMBER OF SEQUENCES: 86
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                43 caccatgaagttottagcagtcotggtactcttgggagtttccatcttctggtctctgc 102
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Length 3376;
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ADDRESSEE: Norris
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Score 64.8; DB 3;
Pred. No. 8.5e-10;
0; Mismatches 87;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                STREET: One Liberty Place, 46th floor CITY: Philadelphia
FILING DATE: 14-MAY-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/971,094
FILING DATE: 30-CCT-1992
PRIOR APPLICATION NUMBER: US 07/888,839
FILING DATE: 27-MAY-1992
PRIOR APPLICATION NUMBER: US 07/805,093
FILING DATE: 11-DEC-1991
ATTORNEY AGENT INFORMATION:
RECISTATION NUMBER: 33,229
REFERENCE/DOCKET NUMBER: TU-1262
TELECOMMUNICATION INFORMATION:
TELEPHONE: (215) 568-3100
TELEFAN: (215) 568-3100
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   COMPUTER: IBM PC COMPATIBLE OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          223 cactgcaaccaccgctgcttctac 246
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ZIF: 19103
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
MINIMER: IBM PC COMPATIBLE
PC-DOS/MS-DY
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             13.8%; 57.4%;
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Best Local Similarity 57.4%
Matches 117; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                       nucleic acid
EDNESS: double
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COUNTRY: USA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ; LOCATION:
US-08-545-860D-29
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       FOPOLOGY:
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APPLICANT: Croce, Carlo
APPLICANT: Canaani, Eli
TILE OF INVENTION: Diagnostics, Therapeutics and Methods
TITLE OF INVENTION: for Detection and Treatment of Acute Leukemias
TITLE OF INVENTION: Resulting from Chromosome Abnormalities in the All-1 Region
NUMBER OF SEQUENCES: 94
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                  ;
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                                                                                                                                                                                                                                                                  Gaps
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                                                                                                                                                                                                                  13.8%; Score 64.8; DB 1; Length 3376; 57.4%; Pred. No. 8.5e-10;
                                                                                                                                                                                                                                                             Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ADDRESSEE: Woodcock, Washburn, Kurtz, Mackiewitz & ADDRESSEE: No. 6040140ris
STREET: One Liberty Place, 46th floor
STREET: Pennsylvania
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SOFTWARE: Patentin Release #1.0, Version #1.25 CURRENT APPLICATION DATA: APPLICATION NUMBER: US/08/545,860D FILING DATE: 07-MAR-1996 CLASSIFICATION: 435
                                                                                                                                                                                                                                                             0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    FILING DATE: 099-DEC-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/327,392
FILING DATE: 19-0CT-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/320,559
FILING DATE: 11-0CT-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/062,443
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PRIOR APPLICATION DATA:
APPLICATION NUMBER: PCT/US94/04496
FILING DATE: 22-APR-1994
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              US-08-545-860D-29/c
: Sequence 29, Application US/08545860D
: Patent No. 6040140
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  223 cactgcaaccaccgctgcttctac 246
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         664 TACTGCTGCTGCTGCTGCTGC 641
                                           TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
                                                                                                                                                                                                                                         Best Local Similarity 57.4 Matches 117; Conservative
  TYPE: nucleic acid
STRANDEDNESS: double
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy COMPUTER: IBM PC COM
                                                                                                        ; NAME/KEY; CDS
; LOCATION: 196..1902
US-08-320-559-29
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                                                                                                                                                                                                                     Query Match
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                                                                                      110.00030101
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COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                     Sequence 4, Application US/08469802B Patent No. 5741645
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      NAME: MUCEING, AND M. REGISTRATION NUMBER: 33,977
REFERENCE/DOCKET NUMBER: 11(
TELECOMMUNICATION: TELEPHONE: 612-305-1217
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             LENGTH: 168 base pairs
TYPE: nucleic acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            INFORMATION FOR SEQ ID NO: SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           612-305-1225
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MEDIUM TYPE: Floppy
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                                                                                                                                                                                                                                                                                                                                                      GENERAL INFORMATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           USA
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US-08-469-802B-4/c
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Best Local Simi
Matches 97;
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Patent No. 6251589
GENERAL INCORMATION:
APPLICANT: TSGJI, Shoji
APPLICANT: SANPEI, Kazujiro
TITLE OF INVENTION: Primers Therefor
TITLE OF INVENTION: Primers Therefor
TITLE OF INVENTION: NUMBER: US/09/043,303
CURRENT APPLICATION NUMBER: US/09/043,303
CURRENT FILING DATE: 1998-05-18
EARLIER PILING DATE: 1996-07-18
NUMBER OF SEQ ID NOS: 17
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59.6%; Pred. No. 2.1e-10;
Live 0; Mismatches 74; Indels
SOFTWAKE: Patentin Release #1.0, Version #1.25 CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                              Ouery Match 13.8%; Score 64.8; DB 5; Best Local Similarity 57.4%; Pred. No. 8.5e-10; Matches 117; Conservative 0; Mismatches 87;
                                       FILING DATE:
CLASS FICATION:
ATORNES/AGENT INFORMATION:
NAME: DELUCA ESQ., MACK
REGISTRATION NUMBER: 33,229
REFERENCE/DOCKET NUMBER: TJU-1242
RELEPHONE: (215) 568-3100
FELEPHONE: (215) 568-3439
INFORMATION FOR SEQ. ID NO: 29:
SEQUENCE CHARACTERISTICS:
LENGTH: 3376 base pairs
                               APPLICATION NUMBER: PCT/US94/04496
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 223 cactgcaaccaccgctgcttctac 246
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   664 TACTGCTGCTGCTGCTGC 641
                                                                                                                                                                                                                                                                                             MOLECULE TYPE: DNA (genomic) FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match 13,7%
Best Local Similarity 59.6°
Matches 109; Conservative
                                                                                                                                                                                                                                              TYPE: nucleic acid
STRANDEDNESS: double
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ; TYPE: DNA
; ORGANISM: p-2093 plasmid
US-09-043-303-7
                                                                                                                                                                                                                                                                                                                           NAME/KEY: CDS
LOCATION: 196..1902
                                                                                                                                                                                                                                                                                 linear
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PCT-US94-04496-29
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APPLICANT: Ranum, Laura P.W.
APPLICANT: Chung, Ming-yi
APPLICANT: Zoghbi, Huda y.
TITLE OF INVENTION: Gene Sequence for Spinocerebellar Ataxia
Patent No. 5741645 13.5%; Score 63.4; DB 1; Length 168; llarity 63.4%; Pred. No. 4.4e-10; Conservative 0; Mismatches 56; Indels (ADDRESSEE: Mueting, Raasch, Gebhardt & Schwappach, STREET: 119 No. 5741645th Fourth Street, Suite 203 CITY: Minneapolis TITLE OF INVENTION: Type 1 and Method for Diagnosis NUMBER OF SEQUENCES: 47
CORRESPONDENCE ADDRESS: SOFTWARE: Patentin Release #1.0, Version #1.25 CURRENT APPLICATION DATA: APPLICATION NUMBER: US/08/469,802B FILING DATE: 06-JUN-1995 CLASSIFICATION: 435

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: MOLECULE TYPE:
US-08-469-802B-5
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     163 GCCCGGAGCCCTGCTGAGGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTTCT 104
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44
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                                                                                                                                                                                                APPLICANT: Orr, Harry T.
APPLICANT: Ranum, Laura P.W.
APPLICANT: Chung, Ming-yi
APPLICANT: Zoghbi, Huda Y.
TITLE OF INVENTION: Gene Sequence for Spinocerebellar Ataxia
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Length 168;
                                                                                                                                                                                                                                                                                                                                                     ADDRESSEE: Mueting, Raasch, Gebhardt & Schwappach, P.A. STREET: P.O. Box 581415
CITY: Minneapolis
STATE: M
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Indels
                                                                                                                                                                                                                                                                                Patent No. 5834183
TITLE OF INVENTION: Type 1 and Method for Diagnosis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            OVERATING SYSTEM: PC_DOS/MS_DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/267,803B
FILING DATE: 28-JUN-1994
CLASSIFIFFARTON.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Score 63.4; DB 2; I
Pred. No. 4.4e-10;
O; Mismatches 56;
                            221 accactgcaaccaccgctgcttctaccactgct 253
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US-08-469-802B-5/c
: Sequence 5, Application US/08469802B
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          NAME: McCormack, Myra H.
REGISTRATION NUMBER: 36,602
REFERENCE/DOCKET NUMBER: 110.
TELECOMMUNICATION INFORMATION:
TELEPHONE: 612-305-1217
TELEFAX: 612-305-1228
                                                                                                                                                                                                                                                                                                                                                                                                                                                     COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-
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INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            LENGTH: 168 base pairs
TYPE: nucleic acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match 13.5
Best Local Similarity 63.4
Matches 97; Conservative
                                                                                                                                                                                                                                                                                                                   NUMBER OF SEQUENCES: 8
CORRESPONDENCE ADDRESS:
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                                                                                                                                 US-08-267-803B-4/c
                                                                                                                                                                                                                                                                                                                                                                                                                       COUNTRY:
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101 gcccagaatccgacaacagctgctccagctgacacgtatccagctactggtcctgctgat 160
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GENERAL.

GENERAL

APPLICANT: Orr, Harry 1.

APPLICANT: Ranum, Laura P.W.

APPLICANT: Chung, Ming-yi

APPLICANT: Coghbi, Huda Y.

TITLE OF INVENTION: Gene Sequence for Spinocerebellar Ataxia

Patent No. 5741645

TITLE OF INVENTION: Type 1 and Method for Diagnosis

TITLE OF INVENTION: Type 1 and Method for Diagnosis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Gene Sequence for Spinocerebellar Ataxia
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                                                                                                                                                              AUDRESSEE: Mueting, Raasch, Gebhardt & Schwappach, STREET: 119 No. 5741645th Fourth Street, Suite 203 (STATE: MN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Type 1 and Method for Diagnosis
                                                                                                                                                                                                                                                                                                                                                                                   OPERATING SYSTEM: PC_DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Score 63.4; DB 1;
Pred. No. 4.4e-10;
0; Mismatches 56;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  221 accactgcaaccaccgctgcttctaccactgct 253
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       REFERENCE/DOCKET NUMBER: 110.00030101
                                                                                                                                                                                                                                                                                                                                                                                                                                           APPLICATION NUMBER: US/08/469,802B
FILING DATE: 06-JUN-1995
CLASSIFICATION: 435
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence 5, Application US/08267803B Patent No. 5834183 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                            E: Floppy disk
IBM PC compatible
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                NAME: Mueting, Ann M.
REGISTRATION NUMBER: 33,977
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TELECOMMUNICATION INFORMATION:
TELEPHONE: 612-305-1217
TELEFAX: 612-305-1225
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        APPLICANT: Orr, Harry T.
APPLICANT: Ranum, Laura P.W.
APPLICANT: Chung, Ming-yi
APPLICANT: Zoghbi, Huda Y.
TITLE OF INVENTION: Gene Seq
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 13.5%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TELEFAX: 612-305-1225
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              171 base pairs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Best Local Similarity 63.49
Matches 97; Conservative
                                                                                                                                                                                                                                                                                                                        COMPUTER READABLE FORM: MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TYPE: nucleic acid
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TITLE OF INVENTION:
NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                                                                 OPERATING SYSTEM:
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101 gcccagaatccgacaacagctgctccagctgacacgtatccagctactggtcctgctgt
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Patent No. 5741645
GENERAL INFORMATION:
APPLICANT: Orr, Harry T.
APPLICANT: Chung, Ming-yi
APPLICANT: Coghbi, Huda Y.
TITLE OF INVENTION: Gene Sequence for Spinocerebellar Ataxia
Patent No. 5741645
TITLE OF INVENTION: Type 1 and Method for Diagnosis
NUMBER OF SEQUENCES: 47
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Length 171;
CORRESPONDENCE ADDRESS:
ADDRESSE: Mueting, Raasch, Gebhardt & Schwappach, P.A.
STREET: P.O. Box 581415
CITY: Minneapolis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CITY: Mineapolis
STATE: MN
STATE: MN
STATE: MN
STATE: MN
STATE: MN
STATE: MN
                                                                                                                           MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/267,803B
FILING DATE: 28-JUN-1994
ATTORNEY APPLICATION: 435
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Score 63.4; DB 2;
Pred. No. 4.4e-10;
0; Mismatches 56;
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                                                                                                                                                                                                                                                                                                                                                                   110.00030120
                                                                                                                                                                                                                                                                                                  ATTORNEY/AGENT INFORMATION:
NAME: MCCOrmack, Myra H.
REGISTRATION NUMBER: 36,602
REFERENCE/DOCKET NUMBER: 110.
TELECOMMUNICATION INFORMATION:
TELEPHONE: 612-305-1217
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  LENGTH: 171 base pairs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match 13.5%
Best Local Similarity 63.4%
Matches 97, Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TYPE: nucleic acid
STRANDEDNESS: single
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CORRESPONDENCE ADDRESS:
ADDRESSEE: Mueting, F
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US-08-267-803B-5
                                                                                                             55458-1415
                                                                                               USA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    APPLICANT: Orr, Harry T.
APPLICANT: Ranum, Laura P.W.
APPLICANT: Chung, Ming-yi
APPLICANT: Zoghbi, Huda Y.
TITLE OF INVENTION: Gene Sequence for Spinocerebellar Ataxia
Patent No. 5834183
TITLE OF INVENTION: Type I and Method for Diagnosis
NUMBER OF SEQUENCES: 85
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ADDRESSEE: Mueting, Raasch, Gebhardt & Schwappach, P.A.
STREET: P.O. Box 581415
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OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
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PatentIn Release #1.0, Version #1.25
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Pred. No. 4.8e-10;
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NAME: MCCOrmack, Myra H.
REGISTRATION NUMBER: 36,602
REFERENCE/DOCKET NUMBER: 110.00030120
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                                               омыев: US/08/469,802B
06-JUN-1995
N. ...
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28-JUN-1994
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                                                                                                            ATTORNEY/AGENT INFORMATION:
NAME: Mueting, Ann M.
REGIGSTRATION NUMBER: 33,977
REFERENCE/COCKET NUMBER: 110.
TELECOMMUNICATION INFORMATION:
TELEPHONE: 612-305-1217
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Best Local Similarity 63.4%;
Matches 97; Conservative C
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INFORMATION FOR SEQ ID NO: 2:
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LENGTH: 195 base pairs
TYPE: nucleic acid
                                    CURRENT APPLICATION DATA:
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COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy
                                                         APPLICATION NUMBER:
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STATE: MN
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                                                                                                CLASSIFICATION:
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US-08-469-8028-2
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Job time: 4146 sec
TELECOMMUNICATION INFORMATION:
TELEPAN: 612-305-1217
TELEPAN: 612-305-1228
TELEPAN: 612-305-1228
TELEPAN: 167-305-1228
TELEPAN: 167-305-1228
LINFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 195 base pairs
TYPE: nucleic acid
STRANDEDNESS: Single
TYPE: nucleic acid
STRANDEDNESS: Single
TYPE: MOLECULE TYPE: DNA
US-08-267-803B-2
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Best Local Similarity 63.49
Matches 97, Conservative
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AC079842 Homo sap1
AC074091 Homo sap1
AX240675 Sequence
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AX240678 Sequence
BDD07430 Reagent a
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Unclassified.
1 (bases 1 to 497)
Edwards, J.-B. Dumas. Milne., Duclert, A. and Bougueleret, L.
                                                                                                                                                                                                                                                                                                                                                                                             AL606742
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Pred. No. 1.6e-96;
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Patent: US 6312922-A 41 06-NOV-2001;
Location/Qualifiers
1. 497
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Sequence 41 from patent US 6312922.
AR177347
AR177347.1 GI:17919702
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RN06295
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138 c 90 g
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14.3 180608
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AR177347
                                                       2002, 04:00:45; Search time 1900.29 Seconds (without alignments) 5186.787 Million cell updates/sec
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                                                                                              US-09-525-361A-23
471
1 ctttgaagcattttgtctg.....aactatgagcgagctaacat 471
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GenCore version 4.5
Copyright (c) 1993 - 2000 Compugen Ltd.
                                                                                                                                                                   1797656 segs, 10463268293 residues
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Maximum Match 100%
Listing first 45 summaries
                                      nucleic search, using sw model
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Match Length DB
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PAT 31-JAN-2002
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)., Rapp, L.R.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          C12N5/10,C12P21/02,C12Q1/68,G01N33/53,C12N15/00,C12N5/00, PC
                                                                                     300
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Gaps
  301 tggtagagtgtgtccctgagatggaatcagcttgagtcttctgcaattgggtcacaacta
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Reagent and method useful in detecting mammary diseases Patent: JP 2001503980-A 4 27-MAR-2001;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              JOHN D KRATOCHVIL, LISA ROBERTS RAPP, JOHN C RUSSELL,
                                                                                                                                                                                                                                                                                          שטיטיא וinear PAT Reagent and method useful in detecting mammary diseases.
BD007431
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Pred. No. 3.5e-96;
2; Mismatches 2;
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    /organism*"unidentified"

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JP 2001503980-A/4
27-MAR-2001
31.0CT-1997 JP 1998520795
31-0CT-1996 US 08/742067
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PC C12N15/09,A61
PC C12N15/10,C12F
A61K37/02
CC Strandedness:
CC Topology: Lir
FH Key
FT Source
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Matches 458; Conservative
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PI JOHI
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AUTHORS
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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                     ctttgaagcalttttgtctgtgctccctgalcttcaggtcaccaccatgaagttcttagc
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Houghton, R.L., Dillon, D.C., Molesh, D.A., Xu, J.,
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Pred. No. 1.6e-96;
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Patent: WO 0175171-A 30 11-OCT-2001;
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Sequence 30 from Patent W00175171.
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/organism="Homo sapiens"
/db_xref="taxon:9606"
137 c 88 g 147
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/organism="unidentified"
/db_xref="taxon:32644"
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Medel, P.A.B., Cohen, M., Colpitts, T.L., Friedman, P.N., Gordon, J.,
Medel, P.A.B., Cohen, M., Colpitts, T.L., Friedman, P.N., Gordon, J.,
Russell, J.C. and Stroupes, S.D.
Reagent and method useful in detecting mammary diseases
ABBOTT LABORATORIES
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C07K16/30,
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JP 2001503980-A/5
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31-0CT-1997 JP 1998520795
31-0CT-1996 US 08/742067
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JP 2001503980-A/5.
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Eukaryota: Metazoa: Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia: Eutheria: Primates: Catarrhini; Hominidae; Homo.
1 (bases 1 to 472)
Billing-Medel, P.A., Cohen, M., Colpitts, T.L., Friedman, P.N.,
Gordon, J., Granados, E.N., Hodges, S.C., Klass, M.R., Kratochvil, J.D.
Roberts-Rapp, L., Russell, J.C. and Stroupe, S.D.
Raagents and methods useful for detecting diseases of the breast
Patent: WO 0165262-A 5 07-SEP-2001;
ABBOTT LABORATORIES (US)
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Pred. No. 3.9e-96;
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/db_xref="taxon:9606"
134 c 86 g 144
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1 (bases 1 to 473)

1 (bases 1 to 773)

1 (bases 1 to 774)

1 (bases 1 to 774)

1 (bases 1 to 773)

2 (bling-Medel, P.A., Cohen, M., Colpitts, T.L., Friedman, P.N., Roborts, Rapp, L., Russell, J.C. and Stroupe, S.D.

Reagents and methods useful for detecting diseases of the breast Patent: WO 0165262-A 6 07-SEP-2001;

ABBOTT LABORATORES (10)
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/db_xref="taxon:9606"
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TGCTCCAGCTGACACGTATCCAGCTACTGGTCCTGCTGATGATGAGGCCCCTGATGCTGA 188
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Catarrhini; Hominidae; Homo,
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Patent: WO 0135811-A 1 25-MAY-2001;
EOS Biotechnology, Inc. (US)
Location/Qualifiers
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/organism="Homo sapiens"
/db_xref="taxon:9606"
a 132 c 88 g 14
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AX328498
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Novel methods of diagnosing and
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Primates;
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Eukaryota; Metazoa;
Mammalia; Eutheria;
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nes 469; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                            actgctcgtaaagacattccagttttacccaaatgggttggggatctcccgaatggtaga 307
418
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98.3%; Pred. No. 4.9e-95;
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CORIXA CORPORATION (US)
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                                                                                                                  AX067322 488 bp
Sequence 26 from Patent W00078960.
AX067322
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/db_xref="taxon:9606"
129 c 84 g 138
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/product="small breast epithelial mucin"
/protein_id="AALO2119.1"
/db_xref="G1:15559111"
/translation="MKFLAVLVLLGVSIFLVSAQNPTTAAPADTYPATGPADDEAPDA
FTTAAPTTATTAATTATTAKDIPVLPKWVGDLPNGRVCP"
117 c 80 g 116 t
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PRI 17-SEP-2001
                                                                                                                                                                                                                                                                                                                                         Biochemistry and Medical Genetics,
770, Bannatyne Avenue, Winnipey, MB R3EOW3,
                                                                                                                 Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 396)
Miksicek, R. J., Myal, Y., Watson, P. H., Murphy, L. C. and Leygue, E.
Identification and characterization of a novel breast-specific
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                musculus
                                                                                                                                                                                                                                                                        2 (bases 1 to 396)
Mikslcek,R.J., Myal,Y., Watson,P.H., Murphy,L.C. and Leygue,E.
Direct Submission
Submitted (23-ANG-2001) Biochemistry and Medical Genetics,
University of Manitoba, 770, Bannatyne Avenue, Winnipeq, MB R3
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              Homo sapiens small breast epithelial mucin mRNA, complete cds. AF414087
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /tissue_type="normal breast tissue and breast tumor"
/note="corresponds to SAGE tag: cttcctgtga (Unigene
HS343493)"
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Pred. No. 4.8e-81;
0; Mismatches 1; Indels
  linear
mRNA
                                                                                                                                                                                                                                                                                                                                                                                                                                            /organism="Homo sapiens"
/db_xref="taxon:9606"
/chromosome="12"
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1. .396
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                                                        AF414087.1 GI:15559110
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Best Local Similarity 99.5%;
Matches 395; Conservative
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Unpublished
AF414087
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C12N15/09, A61K38/00, A61K39/395, A61K39/395, A61P35/00, C07K14/47, 
C07K16/30,
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     Rapp, L.R.
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Granados, E.N., Hodges, S.C., Klass, M.R., Kratochvil, J.D., Russell, J.C. and Stroupe, S.D.
Russell, J.C. and Stroupe, S.D.
Reagent and method useful in detecting mammary diseases
ABDOTT LABORATORIES
ON JUDIO 10503980-A 2 27-MAR-2001;
N. J. 2001503980-A/2
PD 27-MAR-2001
PD 27-MAR-2001
PP 31-CCT-1997 JP 1996520795
PR 31-CCT-1997 US 1996520795
PR 31-CCT-1995 US 08/742067
PP PATRICIA A BILLING MEDEL, MAURICE COHEN, TRACY L. COLPI'
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JULIAN GORDON, EDWARD N GRANADOS, STEVEN C HODGES, PI
                                                                                                                                                                           PI JOHN D KRATOCHVIL, LISA ROBERTS RAPP, JOHN C RUSSELL, STEVEN D STROUPE
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99.3%; Pred. No. 2.2e-61;
iive 0; Mismatches 2;
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/organism="unidentified"
/db_xref="taxon:32644"
a 94 c 65 g 87
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Sequence 3 from Patent W00165262
AX240677
AX240677.1 GI:15797660
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synthetic construct
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1 (bases 1 to 292)
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[ bases 1 to 308)

Billing-Medel,P.A., Cohen,M., Colpitts,T.L., Friedman,P.N., Gordon,J., Granados,E.N., Hodges,S.C., Klass,M.R., Kratochvil,J.D., Roberts-Rapp,L., Russell,J.C. and Stroupe,S.D.

Reagents and methods useful for detecting diseases of the breast Patent: WO 0165262-A 2 07-SEP-2001;

ABBOTT LABORATORIES (US)
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Medel,P.A.B., Cohen,M., Colpitts,T.L., Friedman,P.N., Gordon,J., :
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         DNA
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94 c 65 q 86
                                                                                                AX240676 308 bp
Sequence 2 from Patent WO0165262.
AX240676
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JP 2001503980-A/2.
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Billing-Medel, P.A., Cohen, M., Colpitts, T.L., Friedman, P.N., Cordon, J., Granados, E.N., Hodges, S.C., Klass, M.R., Kratochvil, J.D., Roberts-Rapp, L., Russell, J.C. and Stroupe, S.D. Reagents and methods useful for detecting diseases of the breast, Abatent: WO 0165262-A 3 07-SEP-2001; ABBOTT LABONATORIES (US)
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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/db_xref="taxon:32630"
/note="EST Clone 901429"
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Patent: WO 0135811-A 2 25-MAY-2001;
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Baker, K.P., Goddard, A. and Wood, W.I.
Human polypeptides and methods for the use thereof Patent: WO 0107611-A 220 01-FEB-2001; Genentech, Inc. (US)
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/organism*"Homo sapiens"
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Eukaryota: Metazoa: Chordata; Craniata: Vertebrata: Euteleostomi;
Mammalia: Eutheria: Primates; Catarrhini: Hominidae: Homo.
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Baker.K.P., Goddard,A. and Wood,W.I.
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AAQ84832 AAS83104 AAQ75166

AAV30271 AAV17226 AAA59242 AAA59241

AAX55582 AA291765 AAD18673 AAD18674 AAZ65099 AAF44245

AAF44870 AAV31990 AAX55579 AAD18670

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Breast cancer; diagnosis; prognosis; detection; screening; antibody; oestrogen receptor; anti-oestrogen; immune response; lymph node; metastases; tumour; BCR3; BCQ8; BCQ5; BCH1; BCN1; BCN2; BCN5; BCN2; BCN2; BCN3; BC
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/product= BCHl protein
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DNA encoding novel AF-9 cDNA. Homo s Glutamine rich reg

SCA2 gene CAG repe Exons E, C and A o Exons D, C, B and

ALIGNMENTS

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comprise adding a drug candidate to a cell that expresses a protein selected from BCH1, BCA2, BCJ7, BCN1, BCN5, BCO2, BCO2, BCO2, BCC3, BCR2, BCX2 and BCY3 or their fragments and determining the effect of the drug on the expression of those proteins. Antibodies to breast cancer genes (specifically BCH1 or its fragment (BCH1p1 or BCH1p2)) are useful for inhibiting and treating breast cancer in individuals who are non-responsive to anti-oestrogen and positive for oestrogen receptor. Compositions comprising BCH1 or a nucleic acid encoding in BCH1 are useful for eliciting an immune response in an individual. The antibodies are also useful for the diagnosis and prognosis of breast cancer and for screening compositions which modulate the breast cancer phenotype. The method allows rapid and simple
                                                                                                                                                                                        gene
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                                                                                                                                                                                                                                                   methods for screening drug candidates are described which
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       99.7%; Score 469.4; DB 21.
ilarity 99.8%; Pred. No. 3.4e-119;
Conservative 0; Mismatches 1;
                                                                                                                                                                                                                         Disclosure; Fig 32; 258pp; English
                                                                             (EOSB-) EOS BIOTECHNOLOGY INC
 99US-0440676.
99US-0440677.
99US-0450810.
99US-0453137.
                                                    2000US-0453137.
                                                                                                                              WPI; 2000-638216/61.
P-PSDH; AAB00184.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match
Best Local Similarity
Matches 470; Conserv
                                                                                                        Gish KC;
16-NOV-1999;
16-NOV-1999;
29-NOV-1999;
02-DEC-1999;
                                                    08-MAR-2000;
                                                                                                       Mack D,
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The present sequence encodes a human breast cancer protein, designated BCH1. BCH1 is upregulated in breast cancer tissue, and is found on chromosome 12. cytoband 12q12. BCH1 can be used as an indicator of breast cancer, for determining non-responsiveness to anti-oestrogen therapy and for treating breast cancer. BCH1 nucleic acid is useful for day and single breast cancer, and BCH1 is useful for determining the prognosis of breast cancer and for determining whether an individual with breast cancer will be responsive to anti-oestrogen therapy (where the prognosis and non-responsiveness, respectively. BCH1 is also useful for screening for candidate drugs and bloactive agents. Inhibitors, antibodies and antisense sequences of BCH1 are useful for treating breast cancer. Antibodies to BCH1 are useful for localizing a therapeutic molety (e.g. cytotoxic agent or radioisotope) to breast cancer tissue,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         genes and protein useful for the diagnosis and treatment of breast
                                                                                           Nucleotide sequence of a human breast cancer protein designated BCH1.
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                                                                                                                                                                                                                               "breast cancer protein BCH1"
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                                                                                                                                                                                        Location/Qualifiers
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              BP.
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           AAF85500 standard; cDNA; 471
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99.88;
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47..103
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Matches 470; Conservative
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/*tag=
                                                                                                                                  anti-oestrogen therapy;
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                                                                                                                                                               Homo sapiens
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                                                                                                                                                                                                                                             sig_peptide
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                                      AAF85500;
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This sequence encodes a human breast tumour protein immunogenic fragment of the invention. The polypeptides or nucleic acids encoding them are useful in vaccines and pharmaceutical compositions for manufacture of medicaments for inhibiting the development of breast canner in a patient. They can also be used to treat breast cancer. Antibodies against these polypeptides can be used to detect and monitor progression of breast cancer in patients. Primers and probes derived from the polynucleotides encoding the breast proteins are useful for detection of breast cancer. Peripheral blood cells from a patient incubated in the presence of at least one polypeptide, such that T cells proliferate, are useful in
                                                        180
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                                                                                                                                                                                                                                                                                                                                  in vaccines for immunotherapy,
tgytagagtgtgtccctgagatggaatcagcttgagtcttctgcaattgggtcacaacta
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development; therapy; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              DNA encoding human breast tumour protein immunogenic fragment.
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97US-0998253.
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breast cancer
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24 - DEC - 1997
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manufacture of a medicament for treating breast cancer in a patient. Antigen presenting cells incubated in the presence of at least one polypeptide are also useful for treating breast cancer.
                                                                               agtcctggtactcttgggagtttccatctttctggtctctgcccagaatccgacaacagc
                                                                                                                                               tgctccagctgacacgtatccagctactggtcctgctgatgatgaggccctgatgctga
                                                                                                                                                                               aaccactgctgctgcaactgcgaccactgctgctcctaccactgcaaccaccgctgc
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                                                       Length 480;
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                             Sequence 480 BP; 121 A; 132 C; 87 G; 140 T; 0 other;
                                                     Score 448.4; DB 20;
Pred. No. 2e-113;
0; Mismatches 6;
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98.5%;
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Best Local Similarity 98.5°
Matches 463; Conservative
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breast cancer;
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                                                                                 The present sequence was isolated from a breast tumour cDNA library. It is provided in a specification relating to compounds for immuncherapy and diagnosis of breast cancer. Breast tumour antigens and the polynucleotides that encode them may be used in the production of a pharmaceutical composition to be used in the treatment of breast cancer. Proliferated T cells and incubated antigen presenting cells are also required. The polypeptides and polynucleotides may also be used to
                of a. .
breast
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                                                                                                                                                                                           Sequence 480 BP; 121 A; 132 C; 87 G; 140 T; 0 other;
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2e-113;
6;
                            detection and
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                                                                                                                                                                                                                                   Score 448.4; I
Pred. No. 2e-11
0; Mismatches
            novel isolated polypeptide comprising
                           the
                           breast cancer protein useful in
                                                            Claim 4; Page 74; 95pp; English.
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This sequence represents a nucleic acid molecule which encodes a secreted human protein. The gene number, and the clone it is derived created human protein. The gene number, and the clone it is derived created human protein to the gene to a human immunoglobulin generate fusion proteins y linking to the gene to a human immunoglobulin protein as compared to the human protein only. The invention relates to 87 novel genes and their fragments (nucleic rais sequences: AAX0661-X00724; amino acid sequences AAX061-X00724; amino acid sequences AAX061-X0074; amino acid sequences AAX06101-X00724; amino acid sequences and their acid sequences and protein or gene therappy. Also, pathological conditions e.g. by protein or gene therappy. Also, pathological conditions can be diagnosed by determining the amount of the new polypucketides in a sample or by determining the presence of mutations in the new polymuclectides. Specific uses are described for each of the 87 conditions are acid and time and the presence of mutations in the new polymuclectides. Specific uses are described for each of the 87 conditions are acid and the second second second second and the second secon
    regulation; malabsorption; gastritis; neoplasm
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Ni J, Olse
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, Moore PA,
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Young P;
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1, Shi Y,
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97US-0048350.
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  endocrine; metabolism;
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Ruben SM,
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                                           Homo sapiens
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30.MAY-1997;
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Indels

Length 489;

DB 20;

95.2%; Score 448.4; DB 20; 98.5%; Pred. No. 2e-113; Live 0; Mismatches 6;

Similarity 98.5

Local Simi hes 463;

Best Loca Matches

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Query Match

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30 - MAY - 1997;
30 - MAY - 1997;
30 - MAY - 1997;
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This sequence represents a nucleic acid molecule which encodes a secreted human protein. The gene number, and the clone it is derived from, are detailed in the descriptor line. The gene can be used to generate fusion proteins by linking to the gene to a human immunoglobulin protein as compared to the human protein only.

The invention relates to 87 novel genes and their fragments (nucleic acid sequences: AAXO061:x0074; amino acid sequences AAW57807-W68004) which are useful for preventing, treating or amellorating medical conditions e.g. by protein or gene therapy. Also, pathological conditions can be diagnosed by determining the amount of the new polypeptides in a sample or by determining the presence of mutations in the new polynucleotides. Specific uses are described for each of the 87 polypuncleotides, based on which tissues they are most highly expressed in
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Ni J, Olsen HS;
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Pred. No. 2e-113;
0; Mismatches (
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DW, Moore PA,
, Young P;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                for described uses).
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98.5%;
                   97US-0048188.
97US-0048350.
97US-0048351.
97US-0048352.
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                                                                                                                                         (HUMA-) HUMAN GENOME SCI INC
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30 - MAY - 1997;
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Best Local Simi
Matches 463; (
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97US-0048154. 97US-0048160. 97US-0048186.

30-MAY-1997; 30-MAY-1997; 30-MAY-1997; 30-MAY-1997; 30-MAY-1997;

us-09-525-36la-23.rng

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This sequence encodes a human secreted protein of the invention. The extended cDNAs (or genomic DNAs obtainable from them) may be used to prepare PCR parimers and probes. These are useful for forensic matching or positive identification by DNA sequencing. They may also be used in the positive identification by DNA sequencing. They may also be used in the positive identification of the extended cDNAs are useful in identification of proteins encoded by the extended cDNAs are useful in identification of tissue types or cell species, as well as identifying tissue specific collectification of genes associated with hereditary diseases or drug response. Signal sequences can be used for chromosome mapping and response. Signal sequences from the CDNAs can be used in construction of secretion vectors. Other sequences derived from the extended cDNAs can be used to clone upstram genomic DNA sequences including promoters. This is in turn useful for identifying proteins that interact with promoter constructions several disorders including, but not limited to: cancer, hyperlipidaemia, cardiovascular and neurodegenerative disorders, autoimmune diseases, and mino acidurias, hypoglycaemia, male rat infertility and myopathies.
                                                                                                                                                                                                                                                          Secreted protein; fingerprint identification technique; chromosome mapping; human; hereditary disease; diagnosis; cancer; hyperlipidaemia; cardiovascular; neurodegenerative disorder; therapy; autoimmune disease; rheumatic disease; embryogenic disorder; myopathy; renal lnjury; amino aciduria; hypoglycaemia; male rat infertility; hypertension; ss.
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Secreted protein EST coding sequence 108-002-5-0-F3-FL.
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98US-0081563,
98US-0096116,
98US-0099273.
                                                                                                                           AA240783 standard; DNA; 497
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10-AUG-1998;
04-SEP-1998;
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The present sequence was isolated from a breast tumour cDNA library. It is provided in a specification relating to compounds for immunotherapy
                                                                                                                          tggtagagtgtgtccctgagatggaatcagcttgagtcttctgcaattgggtcacaacta 360
                                                                                                                                                                                                                                   ttcatgcttcctgtgatttcatccaactacttaccttgcctacgatatcccctttatctc 420
                                                                                                                                                                                                                                             A novel isolated polypeptide comprising an immunogenic portion of a breast cancer protein useful in the detection and treatment of breast
                                   ctttgaagcatttttgtctgtgctccctgatcttcaggtcaccaccatgaagttcttagc
                                                                          tgctccagctgacacgtatccagctactggtcctgctgatgatgatgaagccctgatgctga
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                                                                                                                 aaccactgctgctgcaacaactgcgaccactgctgctcctaccactgcaaccaccgctgc
                                                                                                                                                       ttctaccactgctcgtaaagacattccagttttacccaaatgggttggggatctcccgaa
                                                                                                                                                                                                                                                                         Human; breast tumour antigen; cytostatic; immunotherapy;
                                                                                                                                                                                                                                                                                                                                                                                                   cDNA sequence of human breast tumour clone B511S.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          (CORI-) CORIXA CORP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            P-PSDB; AAB28525
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Xu J,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     WO200061756-A2.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                  Homo sapiens
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02-JUL-1999;
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Indels

Length 497;

Score 448.4; DB 20; Pred. No. 2e-113; 0; Mismatches 6;

95.2%; 98.5%;

Best Local Similarity 98.5 Matches 463; Conservative

Query Match

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      polynucleotides that encode them may be used in the production of a pharmaceutical composition to be used in the treatment of breast cancer. Proliferated T cells and incubated antigen presenting cells are also required. The polypeptides and polynucleotides may also be used to produce a vaccine.
                                                                                                                                                                                                                                                                                                                                                                                  Genetic subtraction; DNA microarray analysis; polymerase chain reaction; cancer; B5115; ss.
                                                                                                                     tgctccagctgacacgtatccagctactggtcctgctgatgatgaagcccctgatgctga 180
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                                                                                          aaccactgctgctgcaacaactgcgaccactgctgctcctaccactgcaaccaccgctgc
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and diagnosis of breast cancer. Breast tumour antigens and the
                                                                   DB 21; Length 578;
                                                                                                                                                                                                                                                                                 taatcagittaittittitaaalaaaaaalaactaigagcgagctaaca 470
                                                                                                                                                                                                                                                                                       Indels
                                              88 G; 147 T; 0 other;
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                                                                  Score 448.4; DB 21,
Pred. No. 2.2e-113;
0; Mismatches 6;
                                                                                                                                                                                                                                                                                                                                                                                                                    Location/Qualifiers
63..335
                                              Sequence 578 BP; 206 A; 137 C;
                                                                Query Match
Best Local Similarity 98.5%;
Matches 463; Conservative 0
                                                                                                                                                                                                                                                                                                                               578
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                                                                                                                                                                                                                                                                                                                                                         entry)
                                                                                                                                                                                                                                                                                                                             AA167224 standard; cDNA;
                                                                                                                                                                                                                                                                                                                                                                     B511S cDNA sequence
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                                                                                                                                                                                                                             Identifying tissue (tumour)-specific polynucleotides overexpressed in tissue of interest as compared to control tissue, for detecting cancer cells in patient, comprises DNA microarray analysis or quantitative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          240
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98.5%; Pred. No. 2.2e-113;
Live 0; Mismatches 6;
                                                                                                                               Xu J,
                                                                                                                               DA,
                                                                                                                                                                                                                                                                                                                                  Claim 4; Page 116; 127pp; English.
                                                                                                                               Molesh
20-JUL-2000; 2000US-219862P.
27-JUL-2000; 2000US-221300P.
18-DEC-2000; 2000US-256592P.
                                                                                                                                                                                                                                                                                             polymerase chain reaction
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Best Local Similarity 98.5:
Matches 463; Conservative
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                                                                                   (CORI-) CORIXA CORP
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ВР

AAX55581 standard; DNA; 482

ttcatgcttcctgtgatttcatccaactacttgcctgcgatatccctttatctc

361

tggtagagtgtgtccctgagatggaatcagcttgagtcttctgcaatt.ggtcacaacta 376

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AAX55581
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                                                                                                                                                                                                                                                                                                                     BS106 is a breast tissue gene with which breast cancer and related, diseases are associated. The BS106 polynucleotides AAV31989-V31993 can be detected by BS106 specific polynucleotides or complements acting as useful markers for detection methods. The products and methods can be used for detecting, diagnosing, staging, preventing or treating, or determining predisposition to diseases or conditions of the breast such
                                                                                      ss; human; BS106; breast tissue gene; breast cancer; detection marker.
                                                                                                                                                                                                                                                                       for
                                                                                                                                                                                                                                                                     Detecting BS106 gene products - useful for developing products detecting, staging, preventing, treating or determining predisposition to e.g. breast cancer
                                                                                                                                                                                                                            JD;
                                                                                                                                                                                                                  Friedman PN;
MR, Kratochvil
                                                                                                                                                                                                                                                                                                                                                                                          Sequence 482 BP; 109 A; 136 C; 90 G; 145 T; 2 other;
                                                                                                                                                                                                                Cohen M, Colpitts TL,
s EN, Hodges SC, Klass
ussell JC, Stroupe SD;
                                                                       sednence.
                                                                                                                                                                                                                                                                                                      Claim 1; Page 88; 114pp; English
                                                                     polynucleotide consensus
                 DNA; 482 BP
                                                                                                                                                                                                                                  Russell JC,
                                                                                                                                                             97WO-US19836
                                                                                                                                                                              96US-0742067
                                                    (first entry)
                                                                                                                                                                                                                          Granados EN,
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                                                                                                                                                                                               (ABBO ) ABBOTT LAB.
                 AAV31992 standard;
                                                                                                                                                                                                                Billing-Medel PA,
                                                                                                                                                                                                                                                                                                                                                                             breast cancer.
                                                                                                                                                                                                                                  Roberts-Rapp L,
                                                                                                        Homo sapiens.
                                                                                                                          WO9818945-A1,
                                                                                                                                                          31-OCT-1997;
                                                   25-SEP-1998
                                                                                                                                                                             31-0CT-1996;
                                                                                                                                           07-MAY-1998
                                  AAV31992;
                                                                     BS106
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SS

JD;

Friedman PN;

Colpitts TL, Fr SC, Klass MR, Stroupe SD;

lose, Hodges Russell JC, Cohen M,

Granadose,

(ABBO) ABBOTT LAB Billiing-Medel PA, WPI; 1999-326991/27.

P-PSDB; AAY13466 Roberts-rapp L,

98WO-US22020. 97US-0962094.

19-OCT-1998; 31-OCT-1997;

14-MAY-1999

New isolated BS106 nucleic acids

Query Match
Best Local Similarity 98.98;
Matches 458; Conservative 2

78 121 181 198

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BS106; breast; marker; detection; diagnosis; breast cancer;

Homo sapiens. W09923230-A1

BS106 consensus polynucleotide sequence.

(first

26-JUL-1999

AAX55581;

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Sequences AAX55578-82 represent overlapping polynucleotide sequences of BS106 clones isolated from the breast tissue. The BS106 nucleic acids correspond to a breast tissue gene and can be used as markers for breast tissue disease. The products can be used for detecting, diagnosing, staging, monitoring, prognosticating, preventing or treating, or determining diseases or conditions associated with BS106, especially
                                                                                                                                                                                                                                                                 Gaps
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                                                                                                                                                                    Length 482;
                                                                                                                                                                                          Indels
                                                                                                                           Sequence 482 BP; 109 A; 136 C; 90 G; 145 T; 2 other;
                                                                                                                                                                Score 447; DB 20;
Pred. No. 4.9e-113;
2; Mismatches 2;
Claim 11; Page 89; 105pp; English.
                                                                                                                                                                 94.98;
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Best Local Similarity 98.99
Matches 458; Conservative
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                                                           .;
                               Score 447; DB 19; Length 482;
Pred. No. 4.9e-113;
2; Mismatches 2; Indels
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diseases are associated. The BS106 polynucleotides AAV1369-V31999 can be detected by BS106 specific polynucleotides AAV1369-V31999 can useful markers for detection methods. The products and methods can be used for detecting, diagnosing, staging, preventing or treating or determining predisposition to diseases or conditions of the breast such as breast cancer.
                                               300
                                                                                                                                                                                                                                                                                                                                 ss; human; BS106; breast tissue gene; breast cancer; detection marker.
                                                                                   Lggtagagtgtgtccctgagatggaatcagcttgagtcttctgcaattgggtcacaacta 360
                                                                                                                            257
                                                    related
                                        241 lictaccactgcicgiaaagacaliccagiiltacccaaaigggiiggggaictcccgaa
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MR, Kratochvil
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 BS106 is a breast tissue gene with which breast cancer
                                                                                                                                                                     Sequence 553 BP; 159 A; 144 C; 101 G; 148 T; 1 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Billing-Medel PA, Cohen M, Colpitts TL, I
Gordon J, Granados EN, Hodges SC, Klass I
Roberts-Rapp L, Russell JC, Stroupe SD;
                                                                                                                                                                                                                                                                                                             BS106 polynucleotide clone 1662885 (ii).
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Sequences AAX55578-82 represent overlapping polynucleotide sequences of BS106 clones isolated from the breast tissue. The BS106 nucleic acids correspond to a breast tissue gene and can be used as markers for breast tissue disease. The products can be used for detecting, diagnosing, staging, monitoring, prognosticating, preventing or treating, or determining diseases or conditions associated with BS106, especially
                                       240
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                                                                                                            360
                                                                                                                                           tggtagagtgtgtccctgagatggaatcagcttgagtcttctgcaattgggtcacaacta
                                                                                                                                                                                                                                                                                                                BS106; breast; marker; detection; diagnosis; breast cancer;
                                                                                                                                                                             J.
                                                                                                                                                                                                                                                                                                                                                                                                                                             Friedman PN;
                                                                                                                                                                                                                                                                                                                                                                                                                                             Colpitts TL, Fr
SC, Klass MR,
Stroupe SD;
                                                                                                                                                                                                                                                                                               BS106 consensus polynucleotide sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Claim 11; Page 89; 105pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       New isolated BS106 nucleic acids
                                                                                                                                                                                                                                              ВР
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Russell JC,
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Gaps

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Indels

DB 19; Length 553;

94.9%; Score 446.8; DB 19.98.3%; Pred. No. 5.9e-113; iive 0; Mismatches 7;

Conservative

Query Match Best Local Similarity Matches 462; Conserv

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1; Gaps
                                                   breast specific gene; breast specific marker; BSG; diagnosis;
                                                                                                                                                                                                                                                                                                                                                                                                                         Detecting, diagnosing, monitoring, staging, prognosticating, imaging and treating breast cancer using protein product of breast specific
                                                                                                                        Length 553;
                                                                                                                                                                                                                    Indels
            G; 148 T; 1 other;
                             Score 446.8; DB 20;
Pred. No. 5.9e-113;
0; Mismatches 7;
                                                                                                                                                                                                                                                                                               Human breast specific gene clone Mam002.
           Sequence 553 BP; 159 A; 144 C; 101
                                                                                                                                                                                                                                                                                                                 therapy; Mam002; ss.
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                            94.9%;
ilarity 98.3%;
Conservative
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                                  al Similarity
462; Conserv
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                                                                                                                                                                                                                                                                                                                 breast cancer;
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                                                                                                                                                                                                                                                                                                                            Homo sapiens
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Matches 46
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This sequence represents a breast specific gene (BSG) clone. The BSG sequences are also referred to as breast specific markers (BSM). The invention relates to methods for diagnosing, monitoring, staging, inaging and treating breast cancer (BC). The methods comprise measuring the levels of BSG products in cells, tissues or body fluids of the patient and comparing the measured levels of BSG, with BSG levels of a normal human control. An antibody against the BSG sequences can be labelled and used for imaging BC in a patient. The antibody can be conjugated to a cytotoxic agent, and used for treating BC in a patient.
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                                                                                                                                                                        544;
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                                                                                                                                                                       Score 446.4; DB 21; Length
Pred. No. 7.5e-113;
0; Mismatches 6; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Human BS106 gene-specific full length cDNA,
                   Claim 7; Page 38; 45pp; English.
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i; Conservative
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gene or its fragment which codes for a BS106 polypeptide, useful for he detection of a breast disease such as breast cancer - \,
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Granados EN, Hodges SC, Klass MR, Kratochvil JD, Roberts-Rapp L;
Russell JC, Stroupe SD;
                                                                                                                                                                                                                                                                                                                                                                             Gaps
                                                                                                                                                                                                                                                                                                                                                                                            polynucleotides. The BSI06 polypeptides and antibodies are useful for detecting, diagnosing, staging, monitoring, prognosticating, preventing, treating or determining the predisposition of an individual to diseases and conditions of the breast such as breast cancer. They are also useful in the treatment of tumours or melastases. Polynucleotides of the invention are useful in drug screening and gene therapy. The present sequence is human BSI06 gene specific full length CDNA, expressed sequence tag (EST) clone
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                                                                                                                                                                                        Invention relates to human BS106-specific polypeptides and
                                                                                                                                                                                                                                                                                                                                                 94.7%; Score 446.2; DB 22; Length 472; ilarity 99.1%; Pred. No. 8e-113; Conservative 0; Mismatches 3; Indels 1;
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28-FEB-2001; 2001WO-US06516
                     29-FEB-2000; 2000US-0516444
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